

Figure 1

A

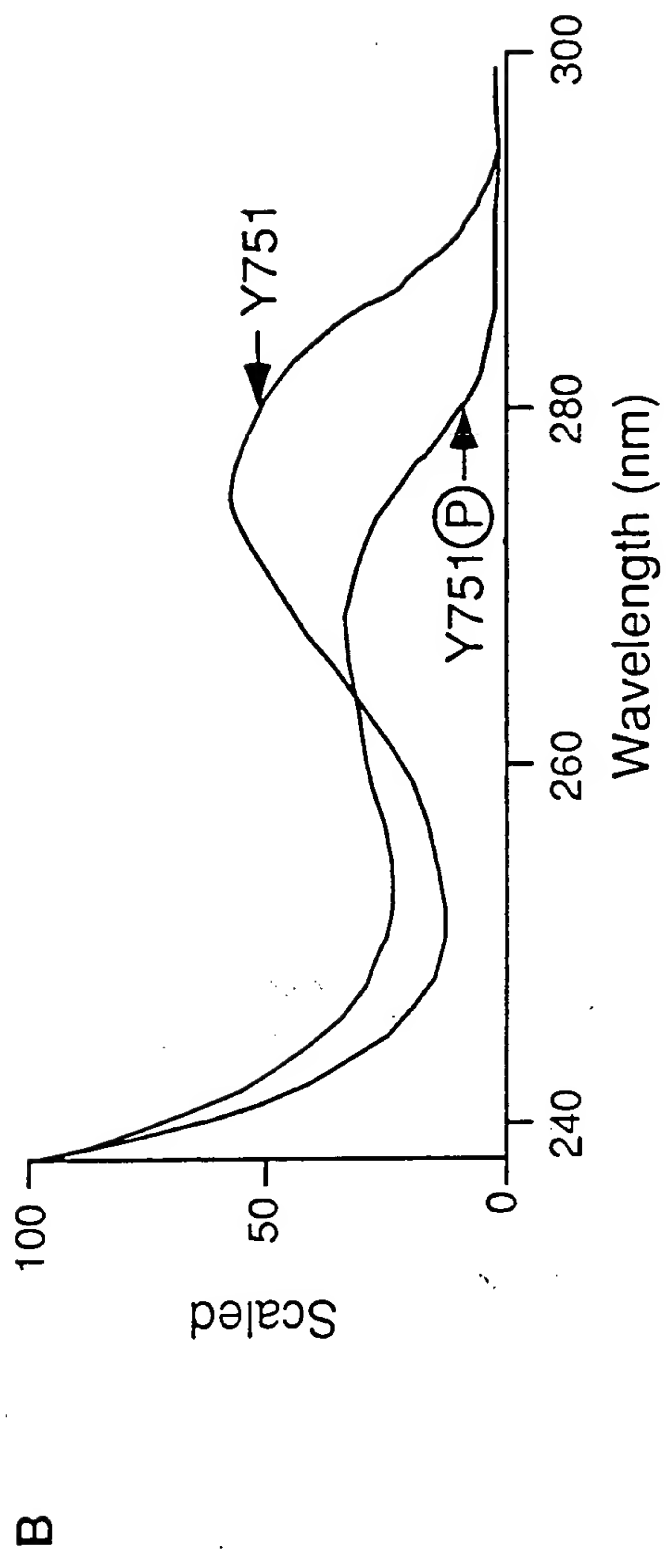


FIG 1 (contd)

C

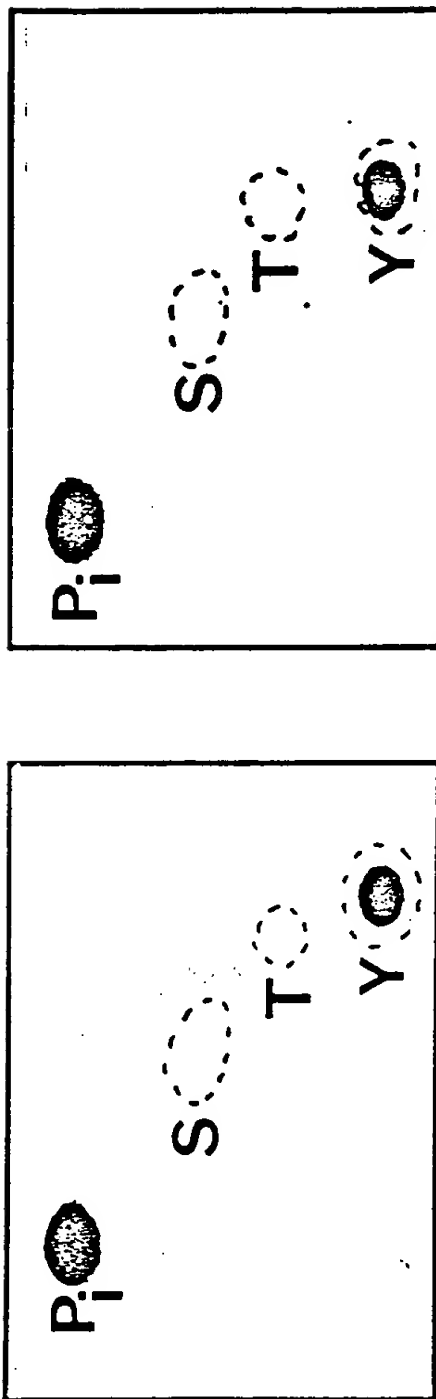
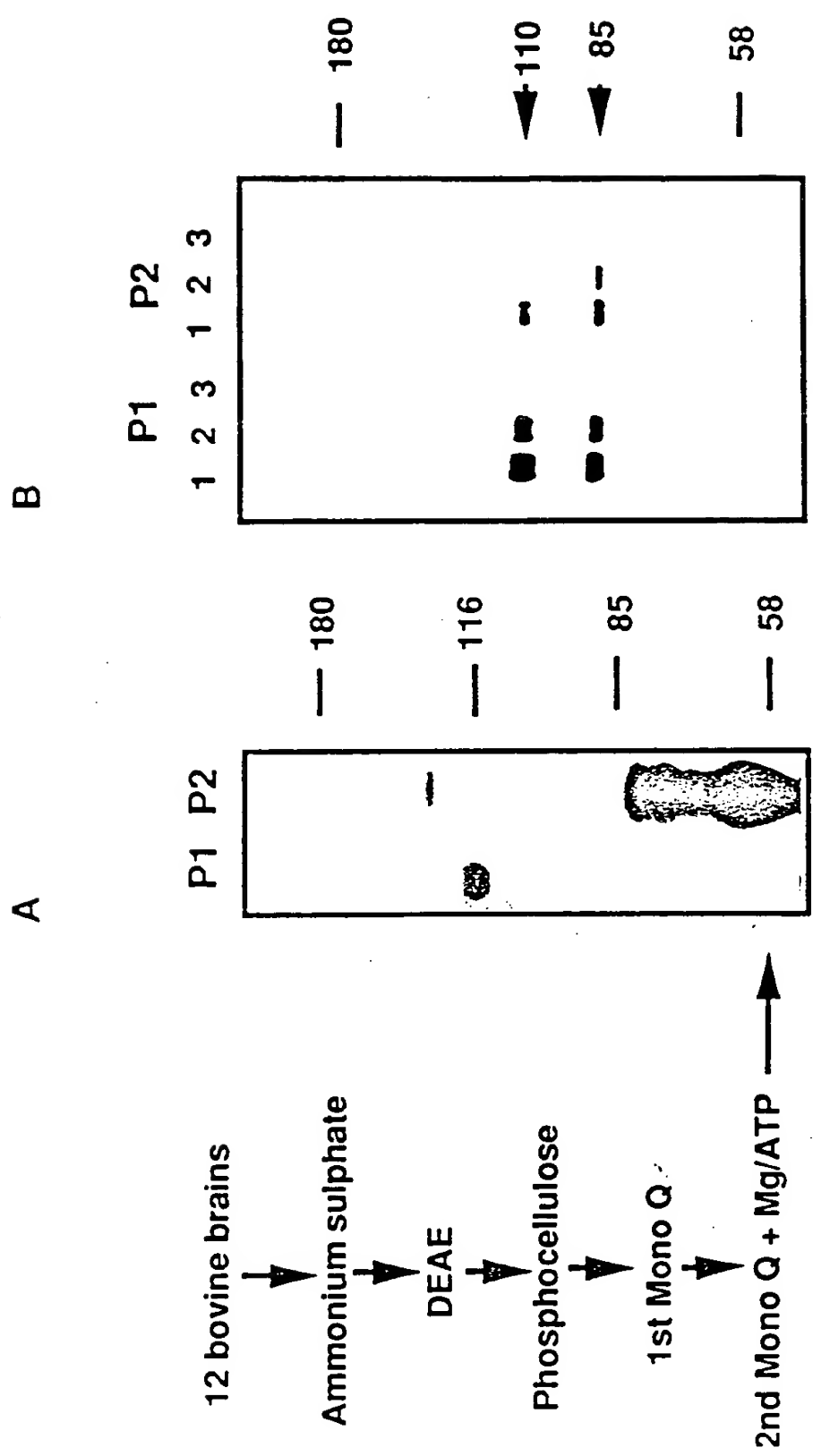


FIG 1 (contd)



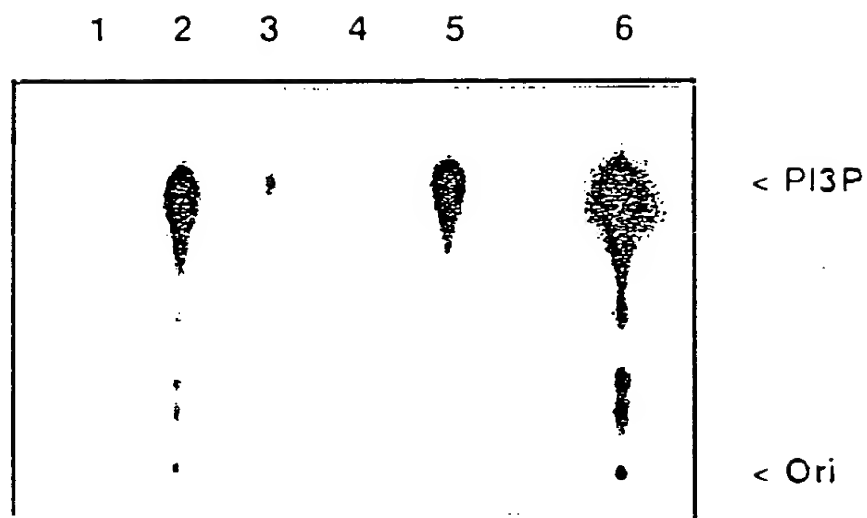
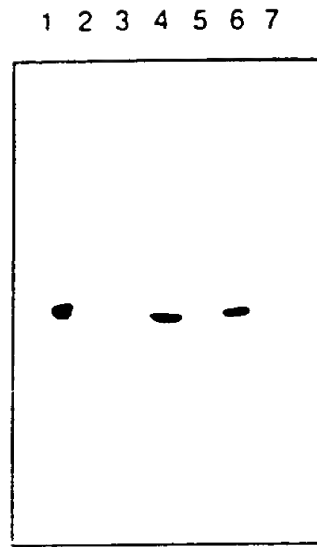


Figure 3

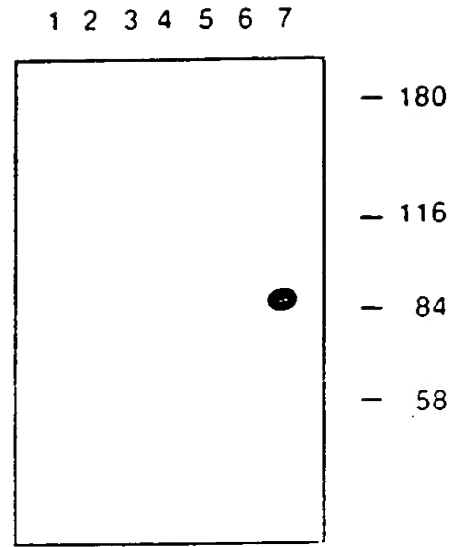
6/80
Figure 4

A



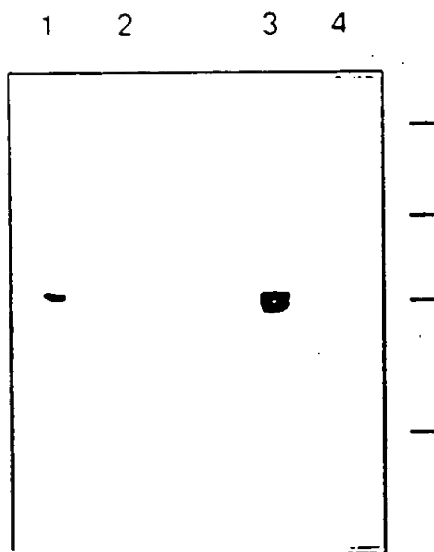
anti-ALPHA

B

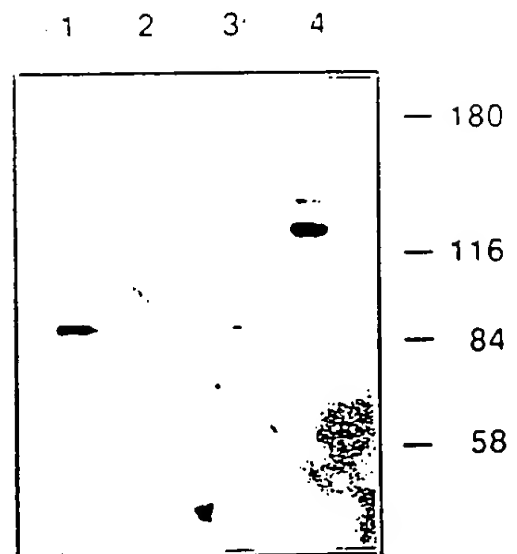


anti-BETA

C



D



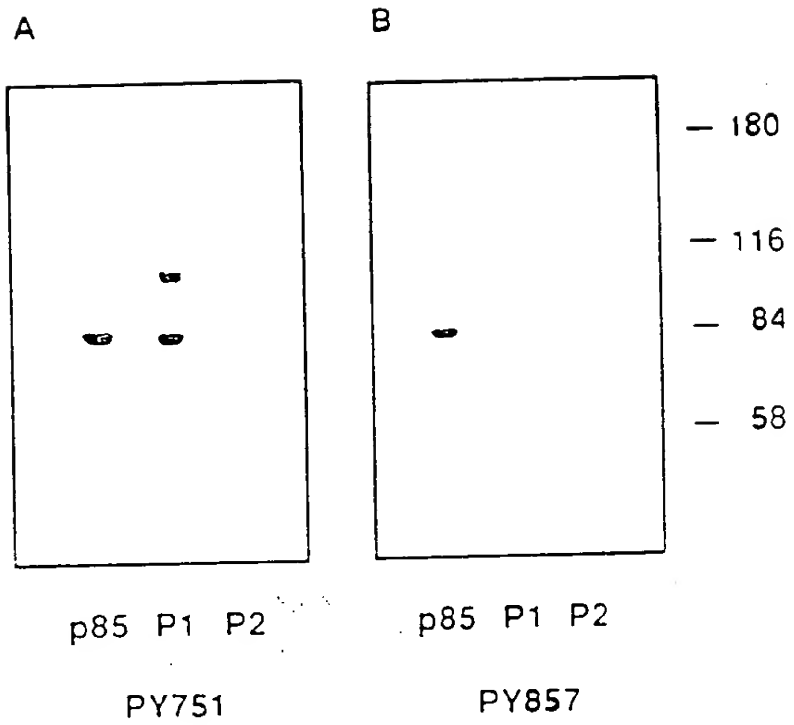
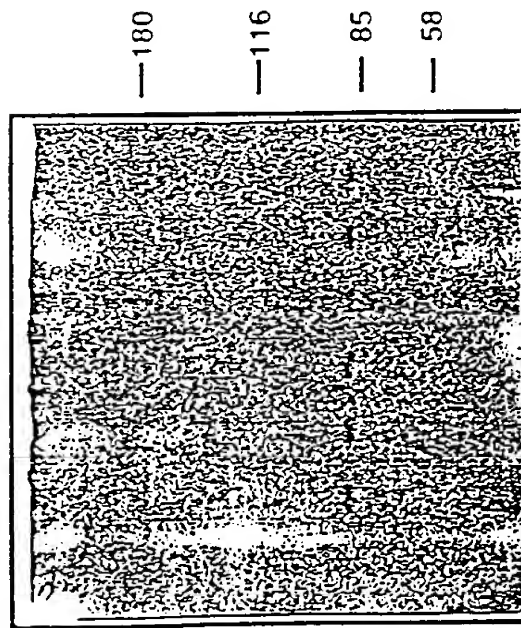


Figure 5

B

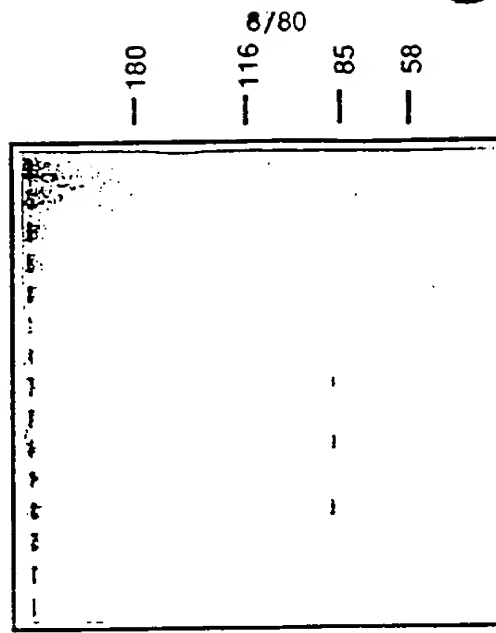
p85 beta



C	Y	Y	Y	Y	Y	Y	Y
O	7	7	8	A	4	5	5
N	5	5	5	T	1	2	7
	1	1	7		6		
							S

A

p85 alpha



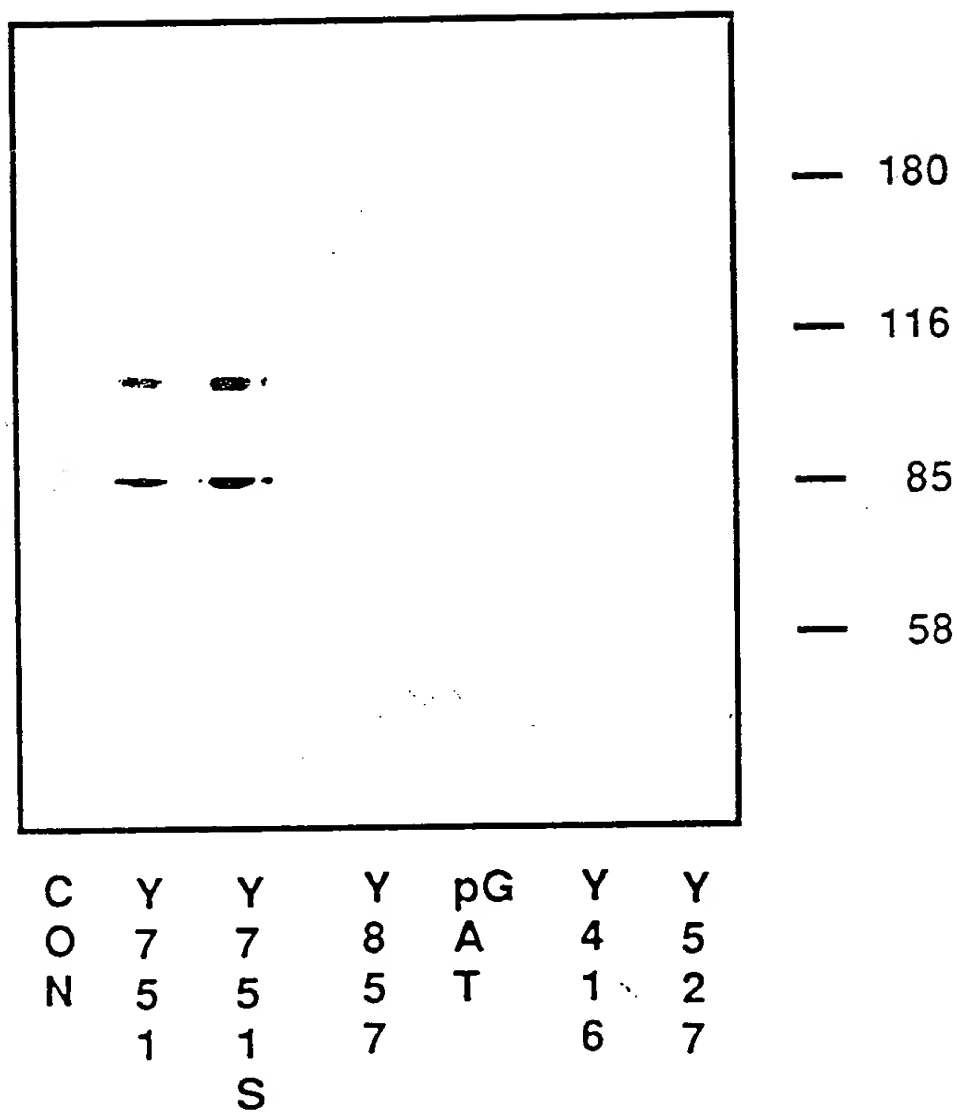
C	Y	Y	Y	Y	Y	Y	Y
O	7	7	8	A	4	5	5
N	5	5	5	T	1	2	7
	1	1	7		6		
							S

Figure 6

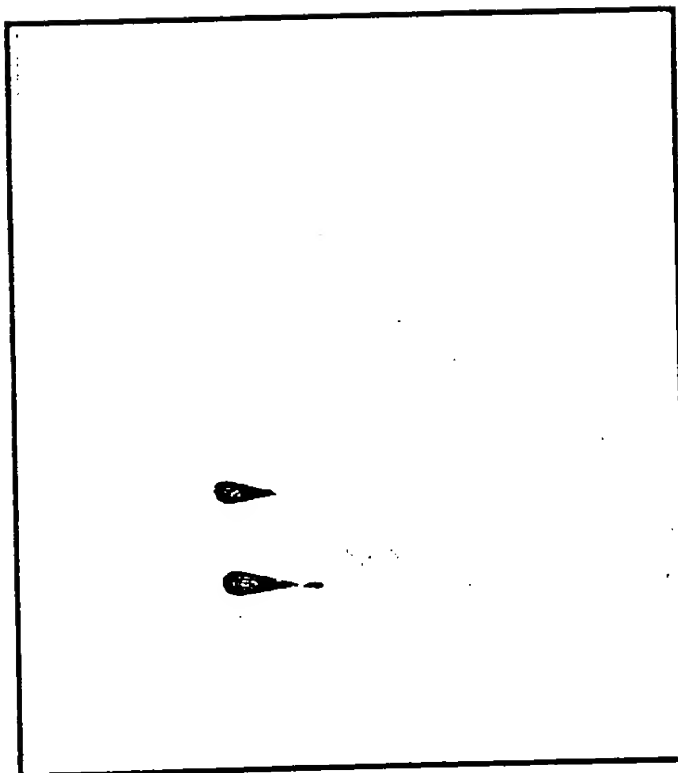
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Figure 7

A



— P13P

1
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C	Y	Y	Y
O	7	7	7
N	5	5	5
	1	1	1
	S		
pG	A	T	
Y	8	5	7
Y	4	1	6
Y	5	2	7

FIG 7 (contd)

11/80

Figure 8

1 2 3 4 5 6



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751	D	M	S	K	D	E	S	V	D	Y	V	P	M	L	D	M	K
751.S				C	D	E	S	V	D	Y	V	P	M	L			
740				G	E	S	D	G	G	Y	M	D	M	S	K		
1313			E	F	C	P	D	P	L	Y	E	V	M	L	K		

Consensus

E	E	E	E	E	Y	M	P	M	X	X
D	D	D	D	D		V				

Figure 9

M P P R P S S G E L W G I H L M 16
ATGCCTCCAAGACCATCATCAGGTGAAGTGGGGCATCCACITGATG 48

P P R I L V E C L L P N G M I V 32
CCCCAAGAATCCTAGTAGAATGTTTACTACCAAAATGGGATGATAGTG 96

T L E C L R E A T L I T I K H E 48
ACTTTAGAATGCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAA 144

L F K E A R K Y P L H Q L L Q D 64
CTATTAAAGAAGCAAGAAATACCTCTCCATCAACTTCTTCAAGAT 192

E S S Y I F V S V T Q E A E R E 80
GAATCTTCTTACATTTTCGTAAGTGTACCCAAGAAGCAGAAAGGGAA 240

E F F D E T R R L C D L R L F Q 96
GAATTTTGTGATGAAACAAGACGACITTTGTGACCTTCGGCTTTTTCAA 288

P F L K V I E P V G N R E E K I 112
CCCTTTTAAAGTAATTGAACCAAGTAGGCAACCGTGAAGAAAGATC 336

L N R E I G F A I G M P V C E F 128
CTCAATCGAGAAATTTGGTTTGTCTATCGGCATGCCAGTGTGTGAATTC 384

D M V K D P E V Q D F R R N I L 144
GATATGGTTAAAGATCCAGAAGTACAGGACITTCGGAAGAAATATCTC 432

FIG 9 (contd)

N V C K E A V D L R D L N S P H 160
 AATGTTGTAAAGAAGCIGTGGATCTTAGGGATCTTAATTCACCTCAT 480
 A
 S R A M Y V Y P P N V E S S P E 176
 AGTAGAGCAATGTATGTTTATCTCTCCAAATGTAGAATCTTCACCAGAA 528
 L P K H I Y N K L D K G Q I I V 192
 CTGCCAAGCACATATATAATAAATTGGATAAAGGGCAATAAATAGTG 576
 V I W V I V S P N N D K Q K Y T 208
 GTGATTTGGGTAATAGTTTCTCCAAATAATGACAAACAGAAAGTATACT 624
 L K I N H D C V P E Q V I A E A 224
 CTGAAATCAACCATGACTGTGTGCCAGAACAAAGTAATTGCTGAAGCA 672
 I R K K T R S M L L S S E Q L K 240
 ATCAGGAAAAAACTCGAAGTATGTTGCTATCATCTGAACAACATAAAA 720
 L C V L E Y Q G K Y I L K V C G 256
 CTCGTGTTTAGAATATCAGGGCAAGTATATTTTAAAAGTGTGTGA 768
 C D E Y F L E K Y P L S Q Y K Y 272
 TGTGATGAATACTTCCTAGAAAAAATATCTCTGAGTCAGTATAAGTAT 816
 I R S C I M L G R M P N L M L M 288
 ATAAGAAGCTGTATAATGCTTGGGAGGATGCCCAATTTCATGCTGATG 864

FIG 9 (contd) A K E S L Y S Q L P M D C F T M 304
GCTAAAGAAAGCCTCTATTCTCAACTGCCAATGGACTGTTTACAATG 912

P S Y S R R I S T A T P Y M N G 320
CCATCATATTCAGAGCGCATCTCCACAGCTACGCCATATATGAATGGA 960

E T S T K S L W V I N S A L R I 336
GAAACATCTACAAAATCCCTTTGGGTATAAATAGTGCACCTCAGAATA 1008

K I L C A T Y V N V N I R D I D 352
AAAATTCTTTGTGCAACCTATGTGAATGTAAATATTTGAGACATTGAC 1056

K I Y V R T G I Y H G G E P L C 368
AAGATTATGTTTCGAACAGGTATCTACCATGGAGGAGAACCCATTATGT 1104

D N V N T Q R V P C S N P R W N 384
GATAATGTGAACACTCAAAGAGTACCTTGTTCCTCAATCCAGGTGGAAT 1152

E W L N Y D I Y I P D L P R A A 400
GAATGGCTGAATTACGATATATACATTCCTGATCTTCCTGCTGCTGCT 1200

R L C L S I C S V K G R K G A K 416
CGACTTTGCCCTTTCCCATTTGTCTGTAAAGGCCGAAGGTGCTAA 1248

E E H C P L A W G N I N L F D Y 432
GAGGAACACTGTCCATTGGCCTGGGGAATATAAATTTGTTGATTAC 1296

FIG. 9 (contd)

T D T L V S G K M A L N L W P V	448
ACAGATACTCTAGTATCTGGAAAATGGCTTTGAATCTTTGGCCAGTA	1344
C	
P H G L E D L L N P I G V T G S	464
OCTCATGGACTAGAAGATTGCTGAACCCCTATTGGTGTACTGGATCA	1392
N P N K E T P C L E L E F D W F	480
AATCCAAATAAAGAACTCCATGTTTAGAGTTGGAGTTTGACTGGTTC	1440
S S V V K F P D M S V I E E H A	496
AGCAGTGTGGTAAAGTTTCCAGATATGTCAGTGATTTGAAGAGCATGCC	1488
N W S V S R E A G F S Y S H A G	512
AATTGGTCTGTATCCCGTGAAGCAGGATTTAGTTATTTCCCATGCAGGA	1536
L S N R L A R D N E L R E N D K	528
CTGAGTAAACAGACTAGCTAGACACAAATGAATTAAGAGAAAATGATAAA	1584
E Q L R A I C T R D P L S E I T	544
GAAACAGCTCCGAGCAATTGTACACGAGATCCTCTATCTGAAATCACT	1632
E Q E K D F L W S H R H Y C V T	560
GAGCAAGAGAAAGATTTTCTGTGGAGCCACAGACACTATTGTGTAAC	1680
I P E I L P K L L L S V K W N S	576
ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTAAATGGAAC	1728

FIG 9 (contd)

R D E V A Q M Y C L V K D W P P 592
 AGAGATGAAGTAGCTCAGATGTAAGTCTTGGTAAAGATTTGGCCTCCA 1776

 I K P E Q A M E L L D C N Y P D 608
 ATCAAGCCTGAACAGGCTATGGAGCCTTCTGGACTGCAATTACCCAGAT 1824

 P M V R G F A V R C L E K Y L T 624
 CCTATGGTTCGAGGTTTTCGCTGTTCGGTCTTAGAAAAATATTTAACA 1872

D
 D D K L S Q Y L I O L V O V L K 640
 GATGACAAACTTTCTCAGTACCTAATTCAGCTAGTACAGGTAATAAAA 1920

 Y E Q Y L D N L L V R F L L K K 656
 TATGAACAGTATTTGGATAACCTGCTGTGTGAGATTTTACTCAAAAAA 1968

E
 A L T N Q R I G H F F F W H L K 672
 GCGTTAACTAATCAAGGATCGGTCACTTTTCTTTTGGCATTTTAAAA 2016

F
 S E M H N K T V S Q R F G L L L 688
 TCTGAGATGCACAATAAAACAGTTAGTCAGAGGTTTGGCCTGCTTTG 2064

G
 E S Y C R A C G M Y L K H L N R 704
 GAGTCCCTATTGCCGTGCATGTGGGATGTATCTGAAGCACCTTAATAGG 2112

G
 Q V E A M E K L I N L T D I L K 720
 CAAGTTGAGGCTATGGAAAAGCTCATTAACCTTGACTGACATTTCTCAAA 2160

FIG 9 (contd) Q E K K D E T Q K V Q M K F L V 736
CAAGAGAAGGATGAACAACACAAAGGTACAGATGAAGTTTTAGTT 2208

E Q M R R P D F M D A L Q G F L 752
GAGCAATGCGGACCAAGATTTCATGGATGCTCTCCAGGGCTTCTG 2256

S P L N P A H Q L G N L R L E E 768
TCTCCTCTAAACCCCTGCTCATCAGCTGGGAAATCTCAGGCTTGAAGAG 2304

C R I M S S A K R P L W L N W E 784
TGTCGAATTATGTCCTCTGCAAAAGGCCACTGTGGTTGAATTGGGAG 2352

N P D I M S E L L F Q N N E I I 800
AACCAGACATCATGTCAGAATTACTCTTTCAGAACAATGAGATCATC 2400

F K N G D D L R Q D M L T L Q I 816
TTTAAATGGGATGATTTACGGCAAGATATGCTAACCCCTTCAGATT 2448

I R I M E N I W Q N Q G L D L R 832
ATTGCCATTATGCAAAATATCTGGCAAAATCAAGTCTTCATCTTCGA 2496

M L P Y G C L S I G D C V G L I 848
ATGTTACCTTATGGATGTCGTCTCAATCGGTGACTGTGTGGGACTTATC 2544

E V V R N S H T I M Q I Q C K G 864
GAGGTGGTGAGAAATTCTCACAATAATGCAGATTCAGTGTAAAGGA 2592

FIG 9 (contd.)

H

G L K G A L O F N S H T L H Q W 880
 GGCCTGAAGGTGCACTGCAGTTTAAACAGCCACACTCCATCAGTGG 2640

L K D K N K G E I Y D A A I D L 896
 CTCAAGACAAGACAAGGGGAAATATATGATGCGGCCATCGATTTC 2688

I

F T R S C A G Y C V A T F I L G 912
 TTTACAGCATCATGTGCTGGATATTGTTGCCACCTTCATTTTGGGA 2736

I G D R H N S N I M V K D D G Q 928
 ATTGGAGATCGTCACAATAGTAATATCATGTGTTAAAGATGATGGACAA 2784

J

L F H I D F G H F L D H K K K 944
 CTGTTTCATATAGATTTTTGGACACTTTTGGATCACAAGAAGAAAAA 2832

K

F G Y K R E R V P F V L T Q D F 960
 TTTGGTTATAACGAGAGCGCGTGCCGTTTGTGTTTGACACAAGATTTC 2880

L I V I S K G A Q E C T K T R E 976
 TTAATAGTGATTAGTAAAGGAGCCCAAGAATGCACAAGACAAGAGAA 2928

F E R F Q E M C Y K A Y L A I R 992
 TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTTCGG 2976

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P110

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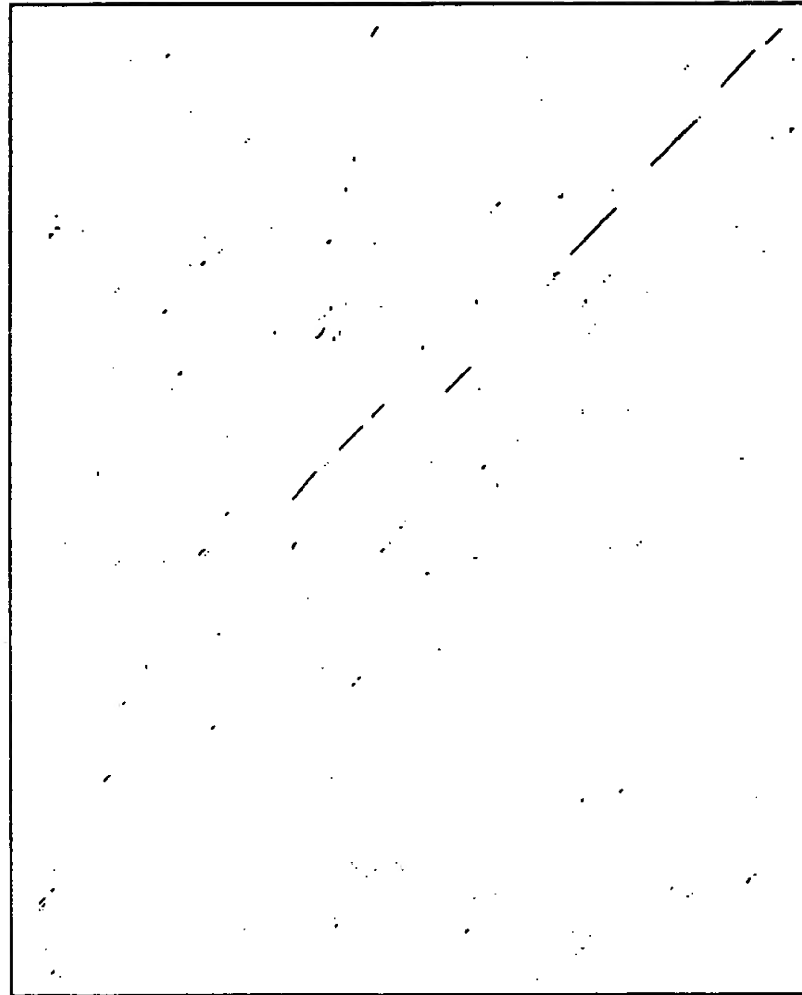


Figure 10 A

```

P110 VCEFD MVKDPEVQDFRRNIILNVCKEAVDLRDLNSPHSRAMYVYPEN 170
      ..| : : | : | : : | : : | : : | : : | : : | : : |
VPS34 NITFCVSQDLDVP.LKVKIKSLEGHKPLLP SQKIINPELMIGSN 49

171 VESSPEL..PKHIYNKLDKGQII VVIWVIVSPNNDKQKYTLKINHDCVPE 218
      | .| : | . : : : | . : : : | : . | : : : : : :
50 VFPSSDLIVSLQVFDKERNRNLTLPIYTPYIPFRNSRTWDYWL..... 92

219 QVIAEAI RKKTRSM LLSSEQL KLCVLEYQ GKYILKVCGCDEYFLEKYPLS 268
      .. : : : : | : | : | : : : | : |
93 .... TLP IRIKQLTFSS.HLR IILWEYNG..... 116

269 QYKYIRSCIMLGRMPNLMIMAKESLYSQLPMDCTMPYSRRISTATPYM 318
      |...| : :
117 .....SKQIPEFF 123

319 NGETSTKSLWINSALRIKILCATYVNVNIRDIDKIYVRTGIYHGGEPLC 368
      | | | . : : : : | : : : : | : : : : | : :
124 NLETSI..FNLKDCITLK.....RGFESLKF RYDVIDHCEVVT 158

369 DNVNTQ RVP CSNPRWNEWLN YDIYIPDL PRAARLC.LSICSVKGRKGAKE 417
      | | : . | | . : : : : | : : | : : : : | : : : :
159 DNKD.....QENLN.KYFQGEFTRLPWLDEITISKLRQRENRT 196

```

Fig 10 B (contd)

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418 .EHCPLAWG.NINLFDYTDTLVSGKMAINLWVPVPHGLEDLINPIGV TGS. 464
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
197 WPQGTFVINLEFPMLELPVVFIEREIMNTQMNIP...TLKNNPGLSTD L 242
      .
465 .NPNKETPCIELEF.DWFSSVVKFPDMSVIEEHANWSVSREAGFSYSHAG 512
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
243 REPNRNDPQIKISLGDKYHSTLKFYD...PDQPNNDPIEEKYRRLERAS 288
      .
513 LSNRLARDNELRENDKEQLRAICTRDPLSEITEQEKFELWSHRHYCVTIP 562
      . . . . . : : : : : : : : : : : : : : : : : : : : : :
289 KNaNLDKQVKPDIKKRDYLNKIINYPPTGKLTAEKGSIWKYRYIIMNNK 338
      .
563 EIIPKLLSVKWSNRDEVAQMYCLVKDWPP IKPEQAMELIDCNYPDPMVR 612
      . | . | | | | . . . . . | : : : : : | . : : : : | : : : : |
339 KALT KLLQSTNLREESERVEVLEIMDSWAEIDIDDALELLGSTFKNLSVR 388
      .
613 GFAVRCLFKYLTDDKLSQYLIQLVQVLKYEQY..... 644
      : : | | . | . | . | . | : : | : : : : : : : : : : :
389 SYAVNRLLKK.ASDKELELYLLQLVEAVCFENLSTFSDKSNSEFTIVDAVS 437
      .
645 .....LDNLLVRFLLKK 656
      : . | . | : : :
438 SQKLSGDSMLLSTSHANQKLLKSISSESETSGTESLPIVISPLAEFLIRR 487

```

[illegible]

Fig 10 B (contd)

954 FVLTOQFLIVISKGAQECTKTREFFERQEMCYKAYLAIRQHANLFINLFS 1003
 :. . . | : . | : . | : . : : : | : . | : . | : . | : . | : .
 763 PIMKLPPIIEAFGGAESS . . NYDKFRSYCFVAYSILRRNAGLILNLF 809
 1004 MMLGSGMPE . . LQSFDDIAYIRKTLALDKTEQEALEYFMKQMNDAHHGGW 1051
 : | . | :
 810 LMKTSNIPDIRIDPENGAILRVREERNLNMSEEDATVHFQNLINDSVNALL 859
 1052 TTKMDWIEHTIKQH 1065
 .. : | : | : : | .
 860 PIVIDH.LHNLAQY 872

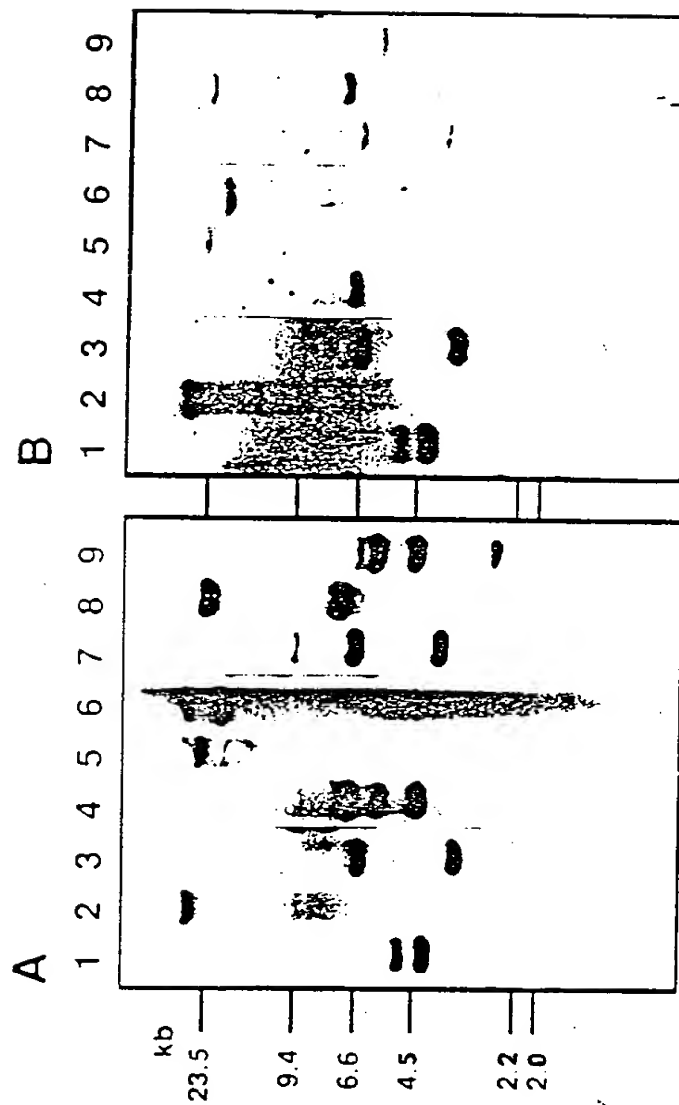


Figure 11

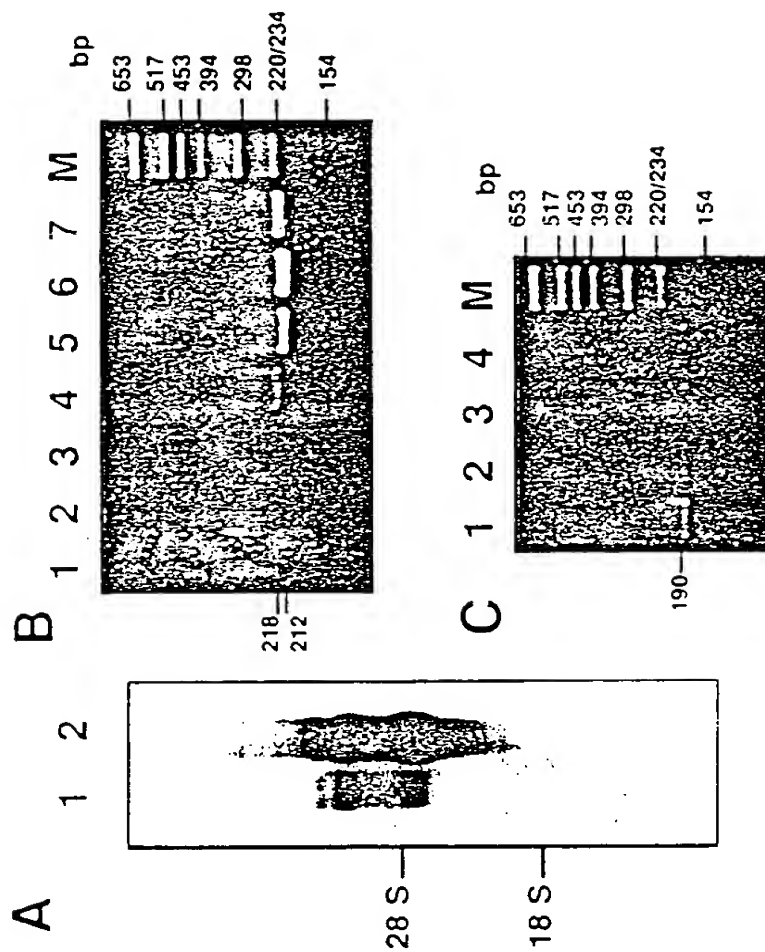


Figure 12

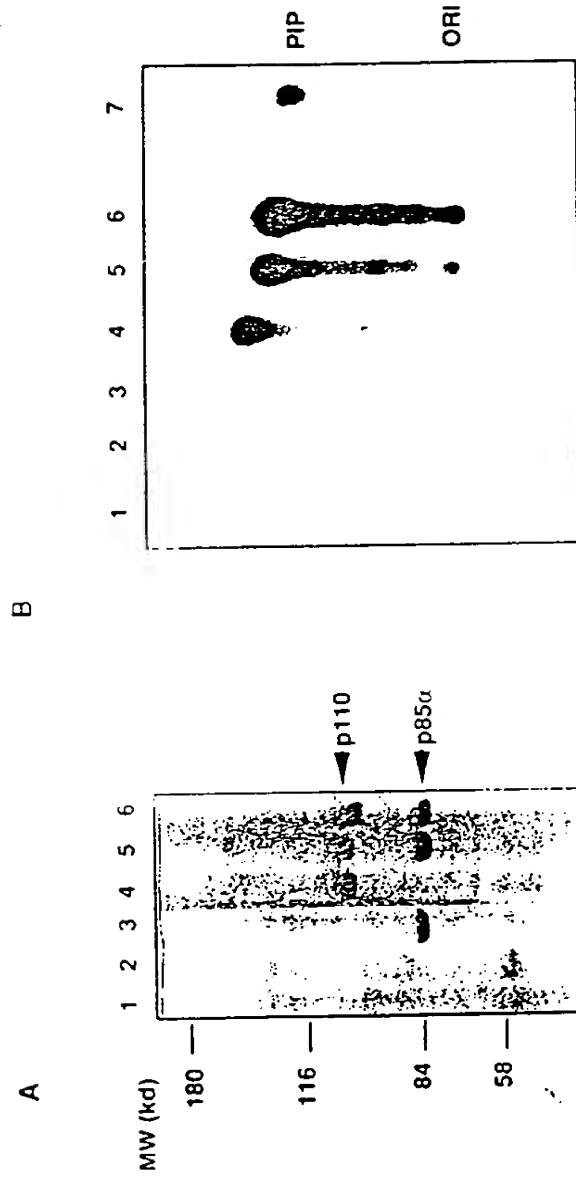


Figure 13

28/80

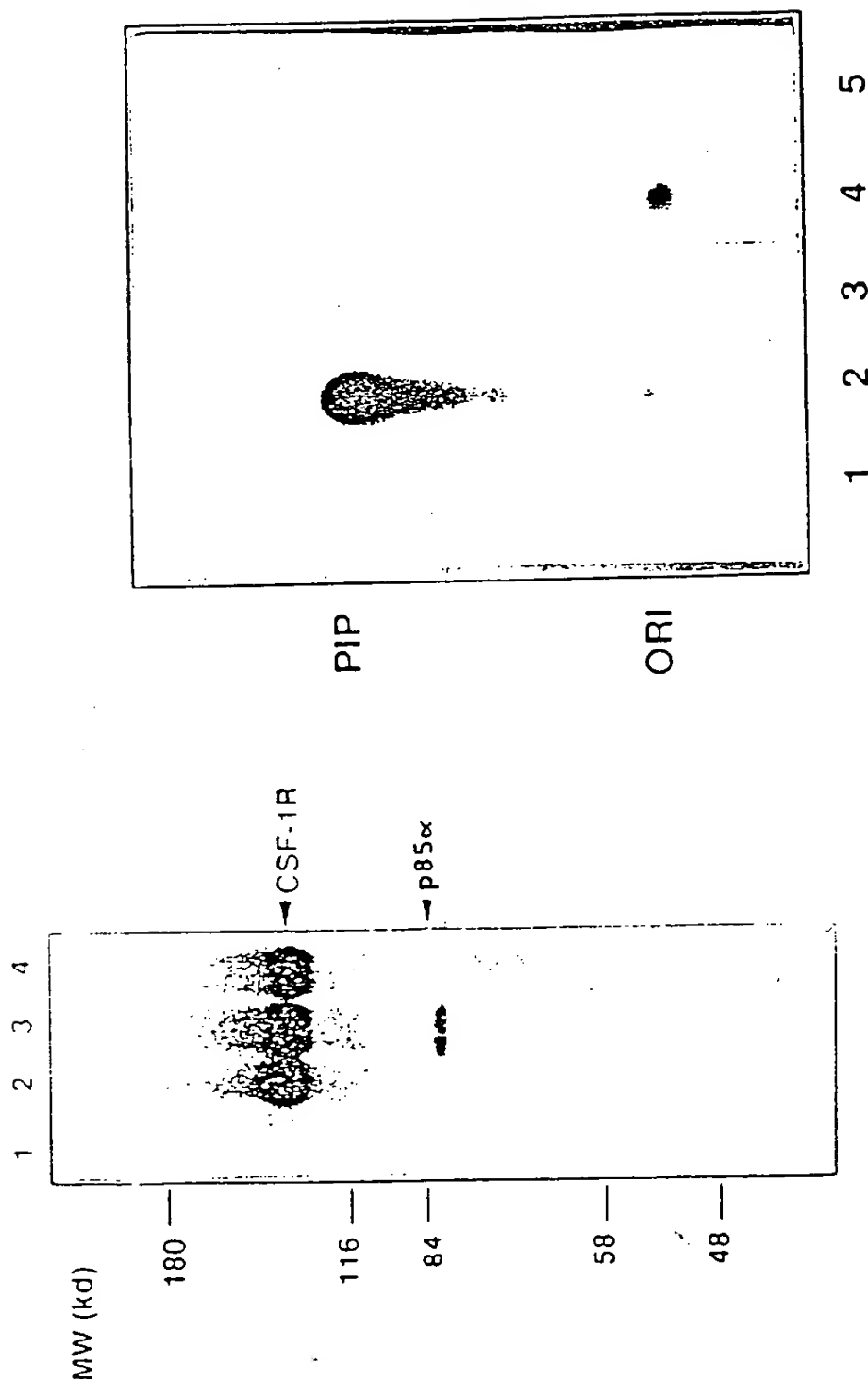
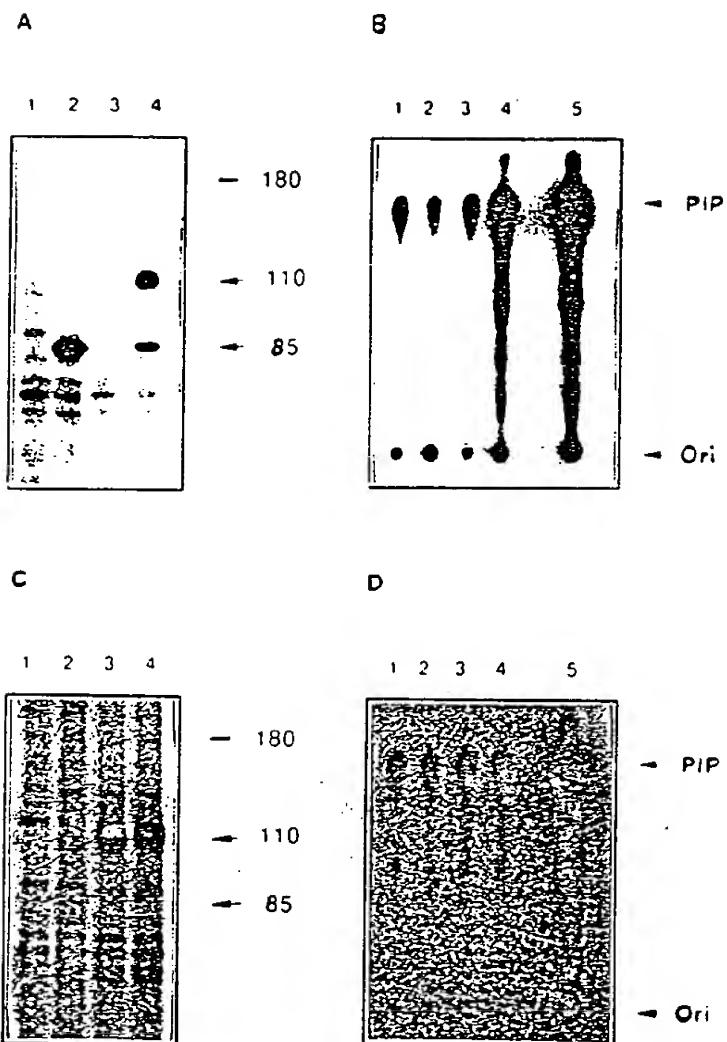


Figure 14

Figure 15



The human p110 cDNA nucleotide and deduced amino acid sequence.

1	ATGCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	48
	-----+-----+-----+-----+-----+-----	
	TACGGAGGTTCTGTAGTAGTCCACTTGACACCCCGTAGGTGAACCTAC	
	M P P R P S S G E L W G I H L M	
49	CCCCAAGAATCCTAGTGGAATGTTTACTACCAAATGGAATGATAGTG	96
	-+-----+-----+-----+-----+-----+-----	
	GGGGTCTTAGGATCACCTTACAAATGATGGTTTACCCTTACTATCAC	
	P P R I L V E C L L P N G M I V	
97	ACTTTAGAAATGCCCTCCGTGAGGCTACATTAGTAACATAAAGCATGAA	144
	---+-----+-----+-----+-----+-----+-----	
	TGAAATCTTACGGAGGCACCTCCGATGTAAATCATTGATATTTCTGACTT	
	T L E C L R E A T L V T I K H E	
145	CTATTTAAGAAGCAAGAAATAACCCCTCTCCATCAACTTCTTCAAGAT	192
	---+-----+-----+-----+-----+-----+-----	
	GATAAATTTCTTCGTTCTTTTATGGGAGAGGTAGTTGAAGAAGTTCTA	
	L F K E A R K Y P L H Q L L Q D	

Figure 16

193 GAATCTTCTTACATTTTCGTAAGTGTTACCCCAAGAACGAGAAAGGAA 240
 -----+-----+-----+-----+-----+-----+
 CTTAGAAGAATGTAAAGCATTCACAATGGGTTCTTCGTCCTTTCCCTT
 E S S Y I F V S V T Q E A E R E
 241 GAATTTTGTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTCAA 288
 -----+-----+-----+-----+-----+-----+
 CTTAAAAACTACTTTGTCTGCTGAACACTAGAACGCCGAAAGTT
 E F F D E T R R L C D L R L F Q
 289 CCATTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAAGAAAAGATC 336
 -----+-----+-----+-----+-----+-----+
 GGTAATAATTTTCATTAACCTTGGTCATCCGTTGGCACTTCTTTCTAG
 P F L K V I E P V G N R E E K I
 337 CTCAATCGAGAAATTGGTTTTTGCTATCGGCATGCCAGTGTCGAATT 384
 -----+-----+-----+-----+-----+-----+
 GAGTTAGCTCTTTAACCAAAACGATAGCCGTACGGTCACACGCTTAAA
 L N R E I G F A I G M P V C E F

FIG 16 (contd)

FIG 16 (contd)

577 GTGATTGGTAATAGTTTCTCCAAATAATGACAAGCAGAAGTATACT
 ---+-----+-----+-----+-----+-----+-----+
 624 CACTAAACCCATTATCAAGAGGTTTACTGTTCGTCCTTCATATGA
 V I W V I V S P N N D K Q K Y T
 625 CTGAAAATCAACCATGACTGTGTGCCAGAACAAAGTAATTGCTGAAGCA
 -----+-----+-----+-----+-----+-----+-----+
 672 GACTTTTAGTTGGTACTGACACACGGTCTTGTTCATTAACGACTTCGT
 L K I N H D C V P E Q V I A E A
 673 ATCAGGAAAAAACTAGAAGTATGTTGCTATCATCTGAACAAATTAAAA
 -----+-----+-----+-----+-----+-----+-----+
 720 TAGTCCTTTTGTGATCTTCATACACGATAGTAGACTTGTAAATTTT
 I R K K T R S M L L S S E Q L K
 721 CTCGTGTTTTAGAATATCAGGGCAAGTACATTTTAAAAAGTGTGTGGA
 -----+-----+-----+-----+-----+-----+-----+
 768 GAGACACAAAATCTTATAGTCCCGTTCCATGTAAAAATTTTCACACACCT
 L C V L E Y Q G K Y I L K V C G

FIG 16 (contd)

769	TGTGATGAATACTTCTAGAAAAATATCCTCTGAGTCAGTATAAGTAT	816
	-+-----+-----+-----+-----+-----+-----	
	ACACTATTATGAAGGATCTTTTATAGGAGACTCAGTCATATTCATA	
	C D E Y F L E K Y P L S Q Y K Y	
817	ATAAGAAGCTGTATAATGCTTGGAGGATGCCCAATTGGAAGATGATG	864
	---+-----+-----+-----+-----+-----+-----	
	TATTCTTCGACATATTACGAACCCCTCCTACGGGTAAACTTCTACTAC	
	I R S C I M L G R M P N L K M M	
865	GCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGACTGTTTACAATG	912
	-----+-----+-----+-----+-----+-----+-----	
	CGATTCTTTCGGAATAAGAGTTGACGGTTACCTGACAAAATGTTAC	
	A K E S L Y S Q L P M D C F T M	
913	CCATCTTATTCAGACGCATTTCCACAGCTACACCATATATGAATGGA	960
	-----+-----+-----+-----+-----+-----+-----	
	GGTAGAATAAGGTCTCGGTAAAGGTGTCGATGTGGTATATACTTACCT	
	P S Y S R R I S T A T P Y M N G	

FIG 16 (contd)

961 GAAACATCTACAAATCCCTTTGGGTTATAAATAGAGCACTCAGAATA
 -----+-----+-----+-----+-----+-----
 CTTGTAGATGTTTAGGGAACCCCAATATTATCTCGTGAGTCTTAT
 E T S T K S L W V I N R A L R I
 1008
 1009 AAAATTCTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGAC
 -+-----+-----+-----+-----+-----+-----
 TTTAAGAAACACGTTGGATGCACCTTAGATTATTAAGCTCTGTAAC TG
 K I L C A T Y V N L N I R D I D
 1056
 1057 AAGATTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCCTTATGT
 ---+-----+-----+-----+-----+-----+-----
 TTCTAAATACAAGCTTGTC CATAGATGGTACCTCCTCTTGGAATACA
 K I Y V R T G I Y H G G E P L C
 1104
 1105 GACAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGAAT
 ---+-----+-----+-----+-----+-----+-----
 CTGTTACACTTGTGAGTTTCTCATGGAACAAGGTAGGGTCCACCTTA
 D N V N T Q R V P C S N P R W N
 1152

FIG 16 (contd)

1153 GAATGGCTGAATTATGATATATACATTCCCTGATCTTCCCTCGTGTGCTGCT
 -----+-----+-----+-----+-----+-----+
 CTTACCGACTTAATACTATATATGTAAGGACTAGAAAGGAGCAGCAGCA
 E W L N Y D I Y I P D L P R A A 1200

 1201 CGACTTTGCCCTTTCCATTGCTCTGTAAAGGCCGAAAGGCTGCTAAA
 -----+-----+-----+-----+-----+-----+
 GCTGAAACGGAAAGGTAAACGAGACAAATTCCGGCTTCCCGCAGATT
 R L C L S I C S V K G R K G A K 1248

 1249 GAGGAACACTGTCCATTGGCATGGGGAATAATAAACTTGTGATTAC
 -----+-----+-----+-----+-----+-----+
 CTCCTTGTGACAGGTAAACCGTACCCCTTTATATTTGAACAACTAATG
 E E H C P L A W G N I N L F D Y 1296

 1297 ACAGACACTCTAGTATCTGGAAAAATGGCTTTGAATCTTTGGCCAGTA
 -----+-----+-----+-----+-----+-----+
 TGTCTGTGATCATAGACCTTTTACCAGAACTTAGAAACCGGTCAT
 T D T L V S G K M A L N L W P V 1344

FIG 16 (contd)

FIG 16 (contd)

1537	CTGAGTAACAGACTAGCTAGAGACAATGAATTAAGGGAAATGACAAA	1584
	---+-----+-----+-----+-----+-----+-----	
	GACTCATTTGCTGATCGATCTCTGTTACTTAATCCCTTTTACTGTTT	
	L S N R L A R D N E L R E N D K	
1585	GAACAGCTCAAAGCAATTCTACACGAGATCCTCTCTCTGAAATCACT	1632
	---+-----+-----+-----+-----+-----+-----	
	CTTGTCGAGTTTCGTTAAAGATGTGCTCTAGGAGAGAGACTTTAGTGA	
	E Q L K A I S T R D P L S E I T	
1633	GAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC	1680
	---+-----+-----+-----+-----+-----+-----	
	CTCGTCCTCTTTCTAAAGATACCTCAGTGTCTGTGATAACACATTGA	
	E Q E K D F L W S H R H Y C V T	
1681	ATCCCCGAAATTCACCCCAAATTGCTTCTGTCTGTAAATGGAATTCT	1728
	---+-----+-----+-----+-----+-----+-----	
	TAGGGGCTTTAAGATGGGTTTAAACGAAGACAGACAAATTTACCTTAAGA	
	I P E I L P K L L L S V K W N S	

FIG 16 (contd)

1729	AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAGATTGGCCTCCA	1776
	-+-----+-----+-----+-----+-----+-----	
	TCTCTACTTCATCGGGTCTACATAACGAACCATTTTCTAACCGGAGGT	
	R D E V A Q M Y C L V K D W P P	
1777	ATCAAACCTGAACAGGCTATGGAACCTCTGGACTGTAATTACCCAGAT	1824
	---+-----+-----+-----+-----+-----+-----	
	TAGTTGGACTTGTC CGATACCTTGAAGACCTGACATTAATGGGTCTA	
	I K P E Q A M E L L D C N Y P D	
1825	CCTATGGTTCGAGGTTTTCGCTGCTTCGGTGCTTGGA AAAATATTAAACA	1872
	---+-----+-----+-----+-----+-----+-----	
	GGATACCAAGCTCCAA AACGACAAGCCACGAACTTTTATATAAATTGT	
	P M V R G F A V R C L E K Y L T	
1873	GATGACAAACTTTCAGTATTTAATTCAGCTAGTACAGGTCCTAAAA	1920
	---+-----+-----+-----+-----+-----+-----	
	CTACTGTTTGAAAGAGTCATAAATTAAGTCGATCATGTCCAGGATTTT	
	D D K L S Q Q Y L I Q L V Q V L K	

FIG 16 (contd)

1921	TATGAACAATATTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA	1968
	-----+-----+-----+-----+-----+-----	
	ATACTTGTTATAAACCTATTGAACGAACACTCTAAAAATGACTTCTTT	
	Y E Q Y L D N L L V R F L L K K	
1969	GCATTGACTAATCAAAGGATTGGGCACCTTTTCTTTTGGCATTTAAAA	2016
	-+-----+-----+-----+-----+-----+-----	
	CGTAACTGATTAGTTTCCTAACCCGTGAAAAAGAAACCGTAAATTTT	
	A L T N Q R I G H F F F W H L K	
2017	TCTGAGATGCACAATAAAACAGTTAGCCAGAGTTTGGCCTGCTTTTG	2064
	---+-----+-----+-----+-----+-----+-----	
	AGACTCTACGTGTTATTTGTCAATCGGTCTCCAACCGGACGAAAC	
	S E M H N K T V S Q R F G L L L	
2065	GAGTCCCTATTGTCGTGCATGTGGGATGTATTGAAGCACCTGAATAGG	2112
	---+-----+-----+-----+-----+-----+-----	
	CTCAGGATAACAGCACGTACACCCCTACATAAACTTCGTGGACTTATCC	
	E S Y C R A C G M Y L K H L N R	

FIG 16 (contd)

FIG 16 (contd)

2305 TGTCGAAATTATGTCTTCTGCAAAAAGGCCACTGTGTTGAATTGGGAG 2352
 -----+-----+-----+-----+-----+-----+-----+
 ACAGCTTAATACAGAAGACGTTTTTCCGGTGACACCAACTTAACCCCTC
 C R I M S S A K R P L W L N W E

 2353 AACCCAGACATCATGTCAGAGTTACTGTTCAGAACAAATGAGATCATC 2400
 -----+-----+-----+-----+-----+-----+
 TTGGGCTCTGTAGTACAGTCTCAATGACAAAGTCTTGTACTCTAGTAG
 N P D I M S E L L F Q N N E I I

 2401 TTTAAAAATGGGATGATTACGGCAAGATATGCTAACACTTCAAATT 2448
 -----+-----+-----+-----+-----+-----+
 AAATTTTACCCCTACTAAATGCCGTTCTATACGATTGTGAAGTTTAA
 F K N G D D L R Q D M L T L Q I

 2449 ATTCGTATTATGGAAAAATATCTGGCAAAATCAAGGCTTGATCTTCGA 2496
 -----+-----+-----+-----+-----+-----+
 TAAGCATAATACCTTTTATAGACCGTTTTAGTTCCAGAACTAGAAGCT
 I R I M E N I W Q Q N Q G L D L R

FIG 16 (contd)

FIG 16 (contd)

FIG 16 (contd)

2881 TTAATAGTGATTAGTAAGGAGGCCCAAGAATGCACAAAGACAAGAGAA
 -----+-----+-----+-----+-----+-----
 AATTATCACTAATCATTTCCCTCGGGTTCTTACGTGTTCTGTTCTCTT
 L I V I S K G A Q E C T K T R E
 2928
 2929 TTTGAGAGGTTTCAGGAGATGTGTTACAAGGCTTATCTAGCTATTCTGA
 -+-----+-----+-----+-----+-----+-----
 AAACCTCTCAAAGTCCTCTACACAAATGTTCGGAATAGATCGATAAGCT
 F E R F Q E M C Y K A Y L A I R
 2976
 2977 CAGCATGCCAATCTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCT
 ---+-----+-----+-----+-----+-----+-----
 GTCGTACGGTTAGAGAAAGTATTTAGAAAAGAGTTACTACGAACCGAGA
 Q H A N L F I N L F S M M L G S
 3024
 3025 GGAATGCCAGAACTACAATCTTTTGATGACATTGCATACATTCGAAAG
 -----+-----+-----+-----+-----+-----+-----
 CCTTACGGTCTTGATGTTAGAAAACCTACTGTAACGTATGTAAGCTTTC
 G M P E L Q S F D D I A Y I R K
 3072

FIG 16 (contd)

FIG 16 (contd)

3265 CTCAGCAGGCAAGACCGATTGCATAGGAATTGCACAATCCATGAACA
-----+-----+-----+-----+-----+-----+
3312 GAGTCGTCGGTTTCTGGCTAACGTATCCCTTAACGTGTTAGGTACTTGT

3313 GCATTAGATTACAGCAAGAACAGAAATAAAATACTATATAATTAA
-----+-----+-----+-----+-----+-----+
3360 CGTAATCTAAATGTCGTTCTTCTTTTATTTATGATATATTAAATTT

3361 TAATGTAAACGCAACAGGGTTTGATAGCAGCTTAAACTAGTTCATTTC
-----+-----+-----+-----+-----+-----+
3408 ATTACATTTGCGTTTGTCCCAAACTATCGTGAATTGATCAAGTAAAG

AAAA
-+-- 3412
TTTT

FIG 16 (contd)

Alignment of human and bovine p110 cDNA nucleotide sequences.

Nucleotide Similarity: 96%

hum110	1	ATGCCTCCAAGACCATCATCAGGTGAAC	TGTGGGCA	TCCACTTGATGCC	50
bov110	1	ATGCCTCCAAGACCATCATCAGGTGAAC	TGTGGGCA	TCCACTTGATGCC	50
	51	CCCAAGAATCCTAGTGGAATGTTACTAC	CAAAATGGA	TGATGACTT	100
	51	CCCAAGAATCCTAGTAGAATGTTACTAC	CAAAATGGG	TGATGACTT	100
	101	TAGAATGCCCTCCGTGAGGCTACATTA	GTAAC	TATAAAGCATGA	150
	101	TAGAATGCCCTCCGTGAGGCTACGTTA	ATAACGATAA	AGCATGA	150
	151	AAAGAAGCAAGAAAATACCCCTCTCCAT	CAACTTCTT	CAAGATGAATCTTC	200
	151	AAAGAAGCAAGAAAATACCCCTCTCCAT	CAACTTCTT	CAAGATGAATCTTC	200

Figure 17

201 TTACATTTTCGTAAGTGTTACCCAAGAACGACAGAAAGGGAATTTTTCG 250
|||||
201 TTACATTTTCGTAAGTGTTACCCAAGAACGACAGAAAGGGAATTTTTCG 250
251 ATGAAACAAGACGACTTTGTGATCTTCGGCTTTTCAACCATTTTAAAA 300
|||||
251 ATGAAACAAGACGACTTTGTGACCTTCGGCTTTTCAACCCCTTTTAAAA 300
301 GTAAATTGAACCAAGTAGGCAACCGTGAGAAAGATCCTCAATCGAGAAAT 350
|||||
301 GTAAATTGAACCAAGTAGGCAACCGTGAGAAAGATCCTCAATCGAGAAAT 350
351 TGGTTTGGCTATCGGCATGCCAGTGTCGGAATTTGATATGGTTAAAGATC 400
|||||
351 TGGTTTGGCTATCGGCATGCCAGTGTCGGAATTCGATATGGTTAAAGATC 400
401 CTGAAGTACAGGACTTCCGAAGAAATATTCTTAATGTTGTAAAGAAGCT 450
|
401 CAGAAGTACAGGACTTCCGAAGAAATATTCTCAATGTTGTAAAGAAGCT 450

FIG 17 (contd)

451	GTGGATCTTAGGGATCTTAATTCAACCTCATAGTAGAGCAATGTATGTCTA	500
451	GTGGATCTTAGGGATCTTAATTCAACCTCATAGTAGAGCAATGTATGTCTA	500
501	TCCGCCACATGTAGAAATCTTCACCAGAGCTGCCAAAGCACATATATAATA	550
501	TCCCTCCAATGTAGAAATCTTCACCAGAACTGCCAAAGCACATATATAATA	550
551	AATTGGATAGAGGCCAAATAAATAGTGGTGATTTGGGTAATAAGTTTCTCCA	600
551	AATTGGATAAAGGCCAAATAAATAGTGGTGATTTGGGTAATAAGTTTCTCCA	600
601	AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCC	650
601	AATAATGACAACACAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCC	650
651	AGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAAGTATGTTGC	700
651	AGAACAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGC	700

701	TATCATCTGAACAAATTAAAACTCTGTGTTTGAATATCAGGGCAAGTAC	750
701	TATCATCTGAACAACTAAAACTCTGTGTTTGAATATCAGGGCAAGTAT	750
751	ATTTTAAAGTGTGTGGATGTGATGAATACTTCTAGAAAATATCCTCT	800
751	ATTTTAAAGTGTGTGGATGTGATGAATACTTCTAGAAAATATCCTCT	800
801	GAGTCAGTATAAGTATAAAGAAAGCTGTATAATGCTTGGAGGATGCCCA	850
801	GAGTCAGTATAAGTATAAAGAAAGCTGTATAATGCTTGGAGGATGCCCA	850
851	ATTGAAGATGATGGCTAAAGAAAGCCTTTATTTCTCAACTGCCAATGGAC	900
851	ATTGATGCTGATGGCTAAAGAAAGCCTCTATTCTCAACTGCCAATGGAC	900
901	TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATA	950
901	TGTTTTACAATGCCATCATATTCCAGACGCATCTCCACAGCTACGCCATA	950

FIG 17. (contd)

52/80

951	TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCAC	1000
951	TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCAC	1000
1001	TCAGAAATAAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGAC	1050
1001	TCAGAAATAAAATTCTTTGTGCAACCTATGTGAATGTAAATATTCGAGAC	1050
1051	ATTGACAAGATTATGTTCGAAACAGGTATCTACCATGGAGAGAACCCCTT	1100
1051	ATTGACAAGATTATGTTCGAAACAGGTATCTACCATGGAGAGAACCCCTT	1100
1101	ATGTGACAAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA	1150
1101	ATGTGATAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA	1150
1151	ATGAATGGCTGAATTATGATATATACATTCCCTGATCTTCCTCGTGTGCT	1200
1151	ATGAATGGCTGAATTACGATATATACATTCCCTGATCTTCCTCGTGTGCT	1200

1201 CGACTTTGCCCTTCCATTGCTCTGTAAAGGCCGAAAGGGTGCTAAAGA 1250
|||||
1201 CGACTTTGCCCTTCCATTGCTCTGTAAAGGCCGAAAGGGTGCTAAAGA 1250
1251 GGAACACTGTCCATTGGCATGGGAAATATAAACTTGTGTGATTACACAG 1300
|||||
1251 GGAACACTGTCCATTGGCCTGGGAAATATAAACTTGTGTGATTACACAG 1300
1301 ACACTCTAGTATCTGGAAAATGGCTTTTGAATCTTTGGCCAGTACCTCAT 1350
|
1301 ATACTCTAGTATCTGGAAAATGGCTTTTGAATCTTTGGCCAGTACCTCAT 1350
1351 GGATTAGAAGATTGCTGAACCCCTATTGGTGTTACTGGATCAAATCCAAA 1400
|||
1351 GGACTAGAAGATTGCTGAACCCCTATTGGTGTTACTGGATCAAATCCAAA 1400
1401 TAAAGAAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450
|||||
1401 TAAAGAAACTCCATGTTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450

1451	TAAAGTTCCAGATAATGTCAAGTGAATGAAGAGCATGCCAATTGGTCTGTA	1500
1451	TAAAGTTCCAGATAATGTCAAGTGAATGAAGAGCATGCCAATTGGTCTGTA	1500
1501	TCCCGAGAAGCAGGATTTAGCTATTCCCAAGCAGGACTGAGTAACAGACT	1550
1501	TCCCGTGAAGCAGGATTTAGTATTCCCATGCAGGACTGAGTAACAGACT	1550
1551	AGCTAGAGACAATGAATTAAGGGAAAATGACAAAAGAACAGCTCAAAGCAA	1600
1551	AGCTAGAGACAATGAATTAAGAGAAAATGATAAAGAACAGCTCCGAGCAA	1600
1601	TTTCTACAGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTT	1650
1601	TTTGTACAGAGATCCTCTATCTGAAATCACTGAGCAAGAGAAAGATTTT	1650
1651	CTATGGAGTCACAGACACTATTGTGTAACATATCCCCGAAATTCTACCCAA	1700
1651	CTGTGGAGCCACAGACACTATTGTGTAACATATCCCCGAAATTCTACCCAA	1700

FIG 17 (contd)

1701 ATTGCTTCTGCTGTTAAATGGAATTCTAGAGATGAAGTAGCCAGATGT 1750
|||||
1701 ATTGCTTCTGCTGTTAAATGGAACTCTAGAGATGAAGTAGCTCAGATGT 1750

1751 ATTGCTTGGTAAAGATTGGCCCTCCAATCAAACCTGAACAGGCTATGGAA 1800
|
1751 ACTGCTTGGTAAAGATTGGCCCTCCAATCAAAGCCTGAACAGGCTATGGAG 1800

1801 CTTCTGGACTGTAAATTACCCAGATCCTATGGTTCGAGGTTTTCGCTGTTCTG 1850
|||||
1801 CTTCTGGACTGCAATTACCCAGATCCTATGGTTCGAGGTTTTCGCTGTTCTG 1850

1851 GTGCTTGGAAAAATATTAAACAGATGACAAACTTTCAGTATTTAATTC 1900
|||||
1851 GTGCTTAGAAAAATATTAAACAGATGACAAACTTTCAGTACCTAATTC 1900

1901 AGCTAGTACAGGTCCCTAAAAATATGAACAATATTGGATAAACTTGCTTGTTG 1950
|||||
1901 AGCTAGTACAGGTACTAAAAATATGAACAGTATTTCGATAAACCTGCTTGTTG 1950

FIG 17 (contd)

1951 AGATTTTACTGAAGAAAGCATTGACTAATCAAAGGATTGGGCACTTTT 2000
||||| ||| ||||| || ||||| ||||| || ||||| |||
1951 AGATTTTACTCAAAAAGCGTTAACTAATCAAAGGATCGGTCACCTTTT 2000
2001 CTTTGGCATTAAATCTGAGATGCACAAATAAAACAGTTAGCCAGAGGT 2050
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2001 CTTTGGCATTAAATCTGAGATGCACAAATAAAACAGTTAGTCAGAGGT 2050
2051 TTGGCCTGCTTTTGGAGTCCTATTGTCCGTGCATGTGGGATGTATTGAAG 2100
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2051 TTGGCCTGCTTTTGGAGTCCTATTGCCC GTGCATGTGGGATGTATCTGAAG 2100
2101 CACCTGAATAGGCAAGTCGAGGCAATGGAAAAGCTCATTAACCTAACTGA 2150
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2101 CACCTTAATAGGCAAGTTGAGGCTATGGAAAAGCTCATTAACCTGACTGA 2150
2151 CATTCTCAAACAGGAGAGGAAGGATGAACACAAAGGTACAGATGAAGT 2200
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2151 CATTCTCAAACAGAGAAAGGATGAACACAAAGGTACAGATGAAGT 2200

FIG 17 (contd)

2201 TTTTAGTTGAGCAAATGAGGCGACCAAGATTTCATGGATGCCCTACAGGGC 2250
|||||
2201 TTTTAGTTGAGCAAATGCGGCGACCAAGATTTCATGGATGCTCTCCAGGGC 2250
|||||
2251 TTGCTGTCTCTAAACCCCTGCTCATCAACTAGGAAACCTCAGGCTTAA 2300
||
2251 TTTCTGTCTCTCTAAACCCCTGCTCATCAGCTGGGAAATCTCAGGCTTGA 2300
|||||
2301 AGAGTGTGCAATTATGTCTTCTGCAAAAAGGCCACTGTGTTGAATTGGG 2350
|||||
2301 AGAGTGTGCAATTATGTCTTCTGCAAAAAGGCCACTGTGTTGAATTGGG 2350
|||||
2351 AGAACCAGACATCATGTGTCAGAGTTACTGTTTCAGAAACAATGAGATCATC 2400
|||||
2351 AGAACCAGACATCATGTGTCAGAAATTAATCTTTTCAGAAACAATGAGATCATC 2400
|||||
2401 TTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACCTTCAAATTAT 2450
|||||
2401 TTTAAAAATGGGGATGATTACGGCAAGATATGCTAACCCCTTCAGATTAT 2450
|||||

FIG 17 (contd)

Year	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

FIG 17 (contd)

59/80

2701	TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCA	2750
2701	TGTGCTGGATAATTGTGTTGCCACCCTTCATTTTGGGAATTGGAGATCGTCA	2750
2751	CAATAGTAACATCATGTGTGAAAGACGATGGACAACCTGTTTCATATAGATT	2800
2751	CAATAGTAATATCATGTGTTAAAGATGATGGACAACCTGTTTCATATAGATT	2800
2801	TTGGACACTTTTGGATCACAAAGAAGAAAATTTGTTTATAAACGAGAA	2850
2801	TTGGACACTTTTGGATCACAAAGAAGAAAATTTGTTTATAAACGAGAG	2850
2851	CGTGTGCCAATTGTTTTGACACACAGGATTTCTTAATAGTGATTAGTAAAGG	2900
2851	CGCGTGCCGTTTGTTTTGACACACAGATTCTTAATAGTGATTAGTAAAGG	2900
2901	AGCCCAAGAATGCACAAGACAAGAGAATTTCAGAGGTTTCAGGAGATGT	2950
2901	AGCCCAAGAATGCACAAGACAAGAGAATTTCAGAGGTTTCAGGAGATGT	2950

FIG 17 (contd)

2951 GTTACAAGGCTTATCTAGCTATTCGACAGCATGCCAATCTCTTCATAAAT 3000
 |||||
 2951 GTTACAAGGCTTATCTAGCTATTCGGCAGCATGCCAATCTCTTCATAAAT 3000
 |||||
 3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTGA 3050
 |||||
 3001 CTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTGA 3050
 |||||
 3051 TGACATTGCATACATTGAAAGACCCCTAGCCTTAGATAAAACTGAGCAAG 3100
 |||||
 3051 TGATATTGCATACATTGAAAGACCCCTAGCCTTAGATAAAACTGAGCAAG 3100
 |||||
 3101 AGGCTTTGGAGTATTTCATGAACAACAAATGAATGATGCACATCATGGTGGC 3150
 |||||
 3101 AGGCTTTGGAGTATTTCATGAACAACAAATGAATGATGCACACCATGGTGGC 3150
 |||||
 3151 TGGACAACAACAAATGGATTGGATCTTCCACACAATTAACAGCATGCATT 3200
 |||||
 3151 TGGACAACAACAAATGGATTGGATCTTCCACACAATTAAGCAGCATGCTTT 3200

60/80

FIG 17 (contd)

3201 GAACTGAAAGATAAACTGAGAAAATGAAAGCTCACTCTGGA

|||||||

3201 GAACTGA.....

FIG 17 (contd)

The alignment between human and bovine p110 proteins.

	10	20	30	40	50	60
h	MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLVTIKHEL	FKEARKYPLHQ				
b	MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLVTIKHEL	FKEARKYPLHQ				
	10	20	30	40	50	60
	70	80	90	100	110	120
h	LLQDESSYIFVSVTQEAERE	EEFFDETRRLCDLRLFQ	FLKVI	EPVGNRE	EKILNREIGFA	
b	LLQDESSYIFVSVTQEAERE	EEFFDETRRLCDLRLFQ	FLKVI	EPVGNRE	EKILNREIGFA	
	70	80	90	100	110	120
	130	140	150	160	170	180
h	IGMPVCEFD	MVKDPEVQD	FRRNILNVCKE	AVDLRDLNSPHSRAM	VYPPHVES	SPPELPKH
b	IGMPVCEFD	MVKDPEVQD	FRRNILNVCKE	AVDLRDLNSPHSRAM	VYPPHVES	SPPELPKH
	130	140	150	160	170	180

Figure 18

190	200	210	220	230	240
h	IYNKLDRGQII	WIVSPNNDKQYTLKINHDCVPEQVIAE	AIKKTRSM	LLSSEQLK	
	:				
b	IYNKLDKGQII	WIVSPNNDKQYTLKINHDCVPEQVIAE	AIKKTRSM	LLSSEQLK	
190	200	210	220	230	240
250	260	270	280	290	300
h	LCVLEYQGKYIL	KVCGCDEYFLEKYP	LSQKYIRSCIM	LGMPNLKMM	AKESLYSQLPMD
b	LCVLEYQGKYIL	KVCGCDEYFLEKYP	LSQKYIRSCIM	LGMPNLKMM	AKESLYSQLPMD
250	260	270	280	290	300
310	320	330	340	350	360
h	CFTMPYSRRRI	STATPYMNGETSTK	SLWVNRALRIKIL	CATYVNVN	LRDIDKIYVRTGI
b	CFTMPYSRRRI	STATPYMNGETSTK	SLWVNRALRIKIL	CATYVNVN	LRDIDKIYVRTGI
310	320	330	340	350	360

FIG 18 (contd)

370	380	390	400	410	420
h	YHGGELCDNVNTQ	RVP	CSNPRWNEWLN	YDIYIPDL	PRAARLCL
					SVKGRKGAKEEHC
b	YHGGELCDNVNTQ	RVP	CSNPRWNEWLN	YDIYIPDL	PRAARLCL
	370	380	390	400	410
					SVKGRKGAKEEHC
					420
430	440	450	460	470	480
h	PLAWGNINLFDY	TD	TLVSGKMALNL	WPVPHGLE	DLNPIG
					VTG
					SNPNKETPCLE
b	PLAWGNINLFDY	TD	TLVSGKMALNL	WPVPHGLE	DLNPIG
	430	440	450	460	470
					VTG
					SNPNKETPCLE
					480
490	500	510	520	530	540
h	SSVVKFPDMSV	IEEHANWS	VSREAGFS	YSHAGLS	NRRLARD
					NELRENDKEQL
					KAISTRDPL
b	SSVVKFPDMSV	IEEHANWS	VSREAGFS	YSHAGLS	NRRLARD
	490	500	510	520	530
					NELRENDKEQL
					KAISTRDPL
					540

FIG 18 (contd)

550	560	570	580	590	600
h	SEITEQEKDFLWSHRHYCVTIPEILPKLLSVKWN	SRDEVAQMYCLVKDW	PIKPEQAME		
b	SEITEQEKDFLWSHRHYCVTIPEILPKLLSVKWN	SRDEVAQMYCLVKDW	PIKPEQAME		
550	560	570	580	590	600
610	620	630	640	650	660
h	LLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLLKKALTN				
b	LLDCNYPDPMVRGFAVRCLEKYLTDDKLSQYLIQLVQVLKYEQYLDNLLVRFLLKKALTN				
610	620	630	640	650	660
670	680	690	700	710	720
h	QRIGHFFFWHLKSEMHNKTVSQRFGLLLESYCRACGMYLKHLNRQVEAMEKLINLTDILK				
b	QRIGHFFFWHLKSEMHNKTVSQRFGLLLESYCRACGMYLKHLNRQVEAMEKLINLTDILK				
670	680	690	700	710	720

	730	740	750	760	770	780
h	QERKDETQKVQMKFLVEQMRP	DFMDALQGLSPLNPAHQ	GNLRLKECRIMSSAKRPLW			
	:					
b	QEKKDETQKVQMKFLVEQMRP	DFMDALQGLSPLNPAHQ	GNLRLKECRIMSSAKRPLW			
	:					

	790	800	810	820	830	840
h	LNWENPDIMSELLFQNN	EIFKNGDDL	RQDMLTLQIIRIMENIWQNGGLDLRMLPYGCLS			
b	LNWENPDIMSELLFQNN	EIFKNGDDL	RQDMLTLQIIRIMENIWQNGGLDLRMLPYGCLS			
	790	800	810	820	830	840

	850	860	870	880	890	900
h	IGDCVGLIEVVRNSHTIMQIQCKGGLKGALQFNSHTLHQWLKDKNKGEIYDA					IDLFTTRS
b	IGDCVGLIEVVRNSHTIMQIQCKGGLKGALQFNSHTLHQWLKDKNKGEIYDA					IDLFTTRS
	850	860	870	880	890	900

FIG 18 (contd)

	910	920	930	940	950	960
h	CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKFGYKRERVPFVLTQDF					
b	CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKFGYKRERVPFVLTQDF					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
h	LIVISKAQECTKTREFFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPQLQSFDDIA					
b	LIVISKAQECTKTREFFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPQLQSFDDIA					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
h	YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNXKITEKMKAHSG					
b	YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNX					
	1030	1040	1050	1060		

FIG 18 (contd)

Figure 19. The predicted amino acid sequence of human p110 CDNA.

```

1  MPPRPSSGEL WGIHIMPRI LVECLLPNGM IVTLECLREA TLVTIKHELF
51  KEARKYPLHQ LLQDESSYIF VSVTQEAERE EFFEETRRLC DLRLFQPFLLK
101 VIEPVGNREE KILNREIGFA IGMPVCEFDN VKDPEVQDFR RNILNVCKEA
151 VDLRDLNSPH SRAMYVYPFH VESSPELPKH IYNKLDRGQI IVVIWIVVSP
201 NNDKQKYTLK INHDCVPEQV IAEAIRKKTR SMLLSSEQLK LCVLEYQGKY
251 ILKVCGCDEY FLEKYPLSQY KYIRSCIMLG RMPNLKMMAK ESLYSQLPMD
301 CFTMPYSRR ISTATPYMNG ETSTKSLWVI NRALRIKILC ATYVNLNIRD
351 IDKIYVRTGI YHGGEPLCDN VNTQRVPCSN PRWNEWLNVD IYIPDLPRAA
401 RLCLSICSVK GRKGAKKEHC PLAWGNINLF DYTDTLVSGK MALNLWPVPH
451 GLEDLNPIG VTGSNPNKET PCLELEFDWF SSVVKFPDMS VIEEHANWSV

```

501 SREAGFSYSH AGLSNRLARD NELRENDKEQ LKAISTRDPL SEITEQEKDF
 551 LWSHRHYCVT IPEILPKLL SVKWSRDEV AQMYCLVKDW PPIKPEQAME
 601 LLDNCNPDPM VRGFAVRCL E KYLTDDKLSQ YLIQLVQVLK YEQYLDNLLV
 651 RFLKKALTN QRIGHFFFWH LKSEMHNKTV SQRFGLLES YCRACGMYLK
 701 HLNROVEAME KLINLTDILK QERKDETQKV QMKFLVEQMR RPDFMDALQG
 751 LLSPLPAHQ LGNLRKECR IMSSAKRPLW LNWENPDIMS ELLEFQNEII
 801 FKNGDDLROD MLTLQIIRIM ENIWQNQGLD LRMLPYGCLS IGDCVGLIEV
 851 VRNSHTIMQI QCKGGLKGAL QFNSHTLHQW LKDKNKGEIY DAAIDLFTRS
 901 CAGYCVATFI LGIGDRHNSN IMVKDDGQLF HIDFGHFLDH KKKKFGYKRE
 951 RVPFVLQDF LIVISKGAQE CTKTREFFERF QEMCYKAYLA IRQHANLEIN
 1001 LFSMMLGSGM PELQSFDDIA YIRKTLALDK TEQEALEYFM KOMNDAHGG
 1051 WTTKMDWIFH TIKQHAIN*

The human PITR-c partial cDNA nucleotide and deduced amino acid sequence.

```

1  GGAGACGACTTCGCACAGATCAACTTATTCTTCAAATCATTTCACTC
   GlyAspLeuArgGlnAspGlnLeuIleLeuGlnIleIleSerLeu
49 ATGGACAAGCTGTACGGAAAGAAATCTGGACTTGAAATTGACACCT
   MetAspLysLeuLeuArgLysGluAsnLeuAspLeuLysLeuThrPro
97 TATAAGGTGTAGCCACCAGTACAAACATGGCTTCATGCAGtTTATC
   TyrLysValLeuAlaThrSerThrLysHisGlyPheMetGlnPheIle
145 CAGTCAGTtCCTGTGGCTGAaGTTCTTGATACAGAGGGAAGCATTCAG
   GlnSerValProValAlaGluValLeuAspThrGluGlySerIleGln
193 AACTTTTTTAGAAAATATGCACCAAGTGAGAATGGCCAAATGGGATT
   AsnPhePheArgLysTyrAlaProSerGluAsnGlyProAsnGlyIle
241 AGTGTGAGGTCATGGACACTtACGTTAAAGCTGTGCTGGATATTGC
   SerAlaGluValMetAspThrTyrValLysSerCysAlaGlyTyrCys
289 GTGATCACCTATATACTTGGAGTTGGAGACAGGCACCTGGATAACCTT
   ValIleThrTyrIleLeuGlyValGlyAspArgHisLeuAspAsnLeu

```

Figure 20

337 TTGCTAACcAAACAGGCAAACTCTTCCACATCGATTTCGGCCAC
LeuLeuThrLysThrGlyLysLeuPheHisIleAspPheGlyHis

FIG 20 (contd)

The human PITR-f partial cDNA nucleotide and deduced amino acid sequence.

```

1  GGGATGACTTACGGCAGGACATGCTAACGCTGCAGATGATTCGCATC
   GlyAspLeuArgGlnAspMetLeuThrLeuGlnMetIleArgIle

49  ATGAGCAAGATCTGGTCCAGGAGGGCTGGACATGCCATGGTCATC
   MetSerLysIleTrpValGlnGluGlyLeuAspMetArgMetValIle

97  TTCCGCTGTTCTCCACCGCGCGGCGAGAGGGATGGTGGAGATGATC
   PheArgCysPheSerThrGlyArgGlyArgGlyMetValGluMetIle

145 CCTAATGCTGAGACCCCTGCGTAAGATCCAGGTGGAGCATGGGTGACC
   ProAsnAlaGluThrLeuArgLysIleGlnValGluHisGlyValThr

193 GGCTCGTTCAAGGACCGGCCCTGGCAGACCGGCTGCAGAAACAACAAC
   GlySerPheLysAspArgProLeuAlaAspArgLeuGlnLysHisAsn

241 CCTGGGAGGACGAGTATGAGAAGGCTGTGGaGAACCTTATCTACTCC
   ProGlyGluaspGluTyrGluLysAlaValGluAsnPheIleTyrSer

289 TCGGCTGGCTGCTGCGTGCCACGTACGTCTTGGGCATCTGTGACCga
   CysAlaGlyCysCysValAlaThrTyrValLeuGlyIleCysAspArg

```

Figure 21

337 CATAATGACAACATCATGCTGAAGACCACCTGGTCACATGTTCCACATC
HisAsnAspAsnIleMetLeuLysThrThrGlyHisMetPheHisIle

385 GACTTCGGC
AspPheGly

FIG 21 (contd)

ALIGNMENT OF HUMAN P110, HUMAN PI-3 KINASE RELATED GENES PITR-C AND PITR-F AND YEAST PI-3 KINASE VPS34.

In upper case are shown amino acids that are conserved in 3 or more of the proteins. Underlined are the residues involved in ATP binding.

	1	50
vps34	GDDLRRQDqLvVQIIslMnellknEnvDLkLtPYkiLaTGpqeGaIEfIpN	
PITR-c	GDDLRRQDqLiLQIIslMdkllrkEnLDLkLtPYkvLaTstkhGFmqfIqs	
hump110	GDDLRRQDmLtLQIIriMeniwqnqgDLrMlPYgcLsiGdcvGLIEvVrN	
PITR-f	GDDLRRQDmLtLQmIriMskiwvqEgLDmMrMviFrcFSTGrgrGMVEmIpN	
Consensus	GDDLRRQD-L-LQII--M-----E-LDL---PY--L-TG---G-IE-I-N	
	51	100
vps34	dtlasilskyhGIlGy.....LklhypdeNatlgVqgwvldnFVksCA	
PITR-c	vpvaevldtegsIqnf.....FrkYapseNgpngIsaevmDtYVksCA	
hump110	shtimqicqkgGlkGalqfnshLtLhqWlkdkNkge.IydaaiDLftrSCA	
PITR-f	aetlrkiqvehGVtGs..fkdrpLadrLqkhNpgedeyekavEnFIYSCA	
Consensus	-----GI-G-----L-----N-----I-----D-FV-SCA	

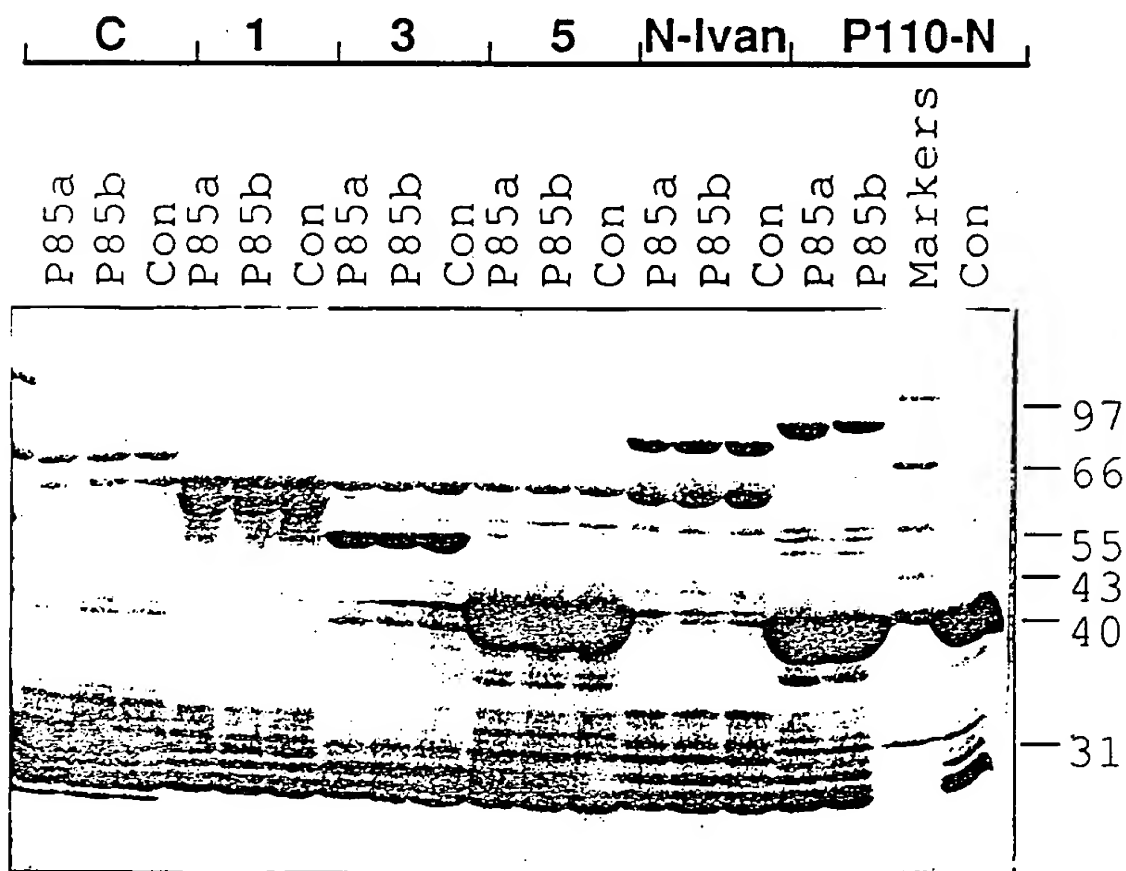
Figure 22

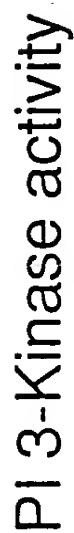
	101		133
vps34		GYC <i>V</i> iTYILGVGDRHLDNLLvtpdGhFFHaDEG	
PITR-c		GYC <i>V</i> iTYILGVGDRHLDNLLtktGkLFHIDEF	
hump110		GYC <i>V</i> aTFILGIGDRHnsNiMvkddGqLFHIDEF	
PITR-f		GCC <i>V</i> aTYVLGICDRHnDNiMlktGhMFHIDEF	
Consensus		GYCV-TYILG-GDRH-DN-----G-LFHIDEF	

FIG 22 (contd)

Figure 23 A

MAPPING THE P85 BINDING SITE ON P110





P85 association

P110N

N-IVAN



3

LD

Figure 24

Mapping of the P85 Binding Site on P110

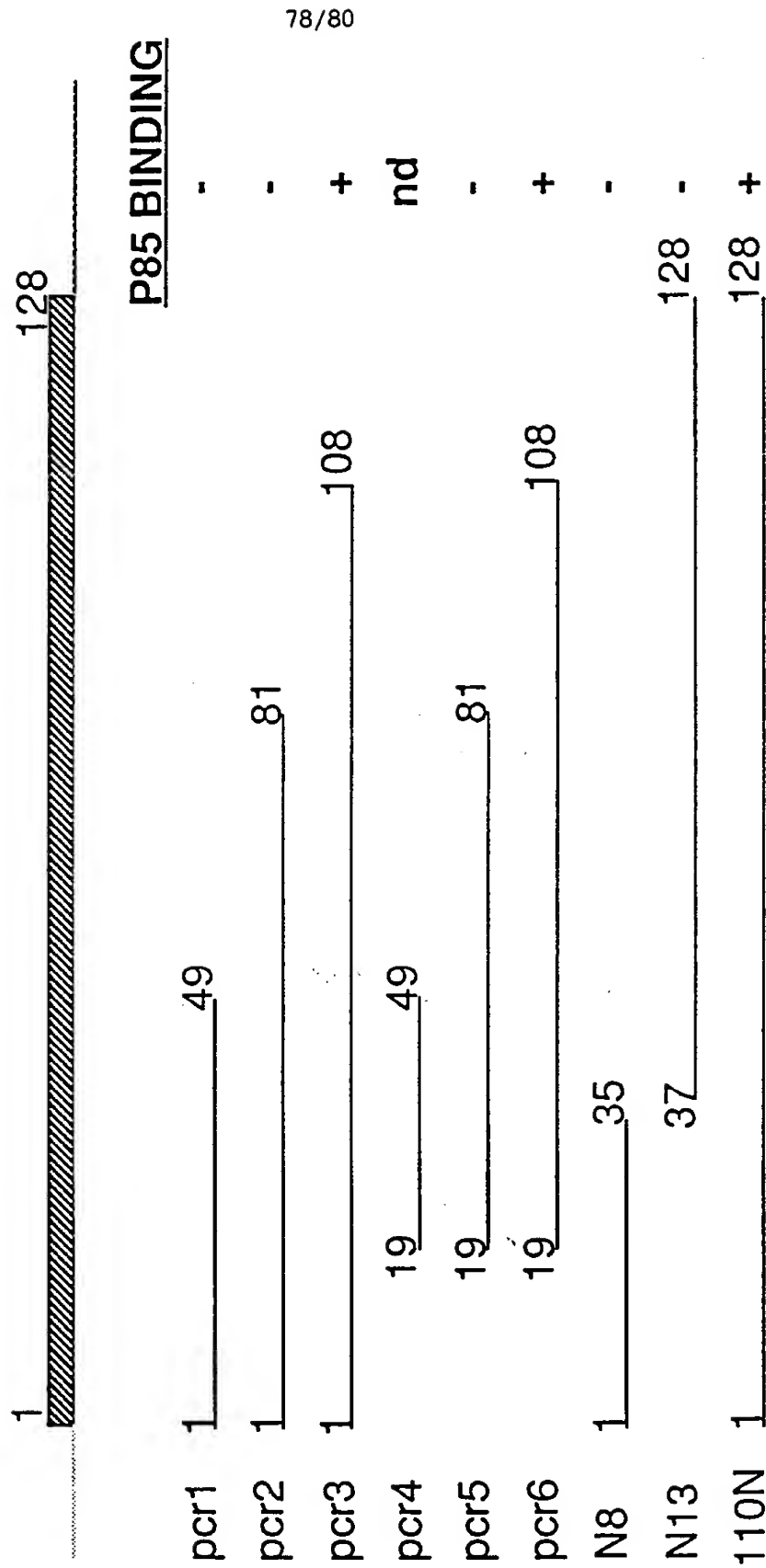
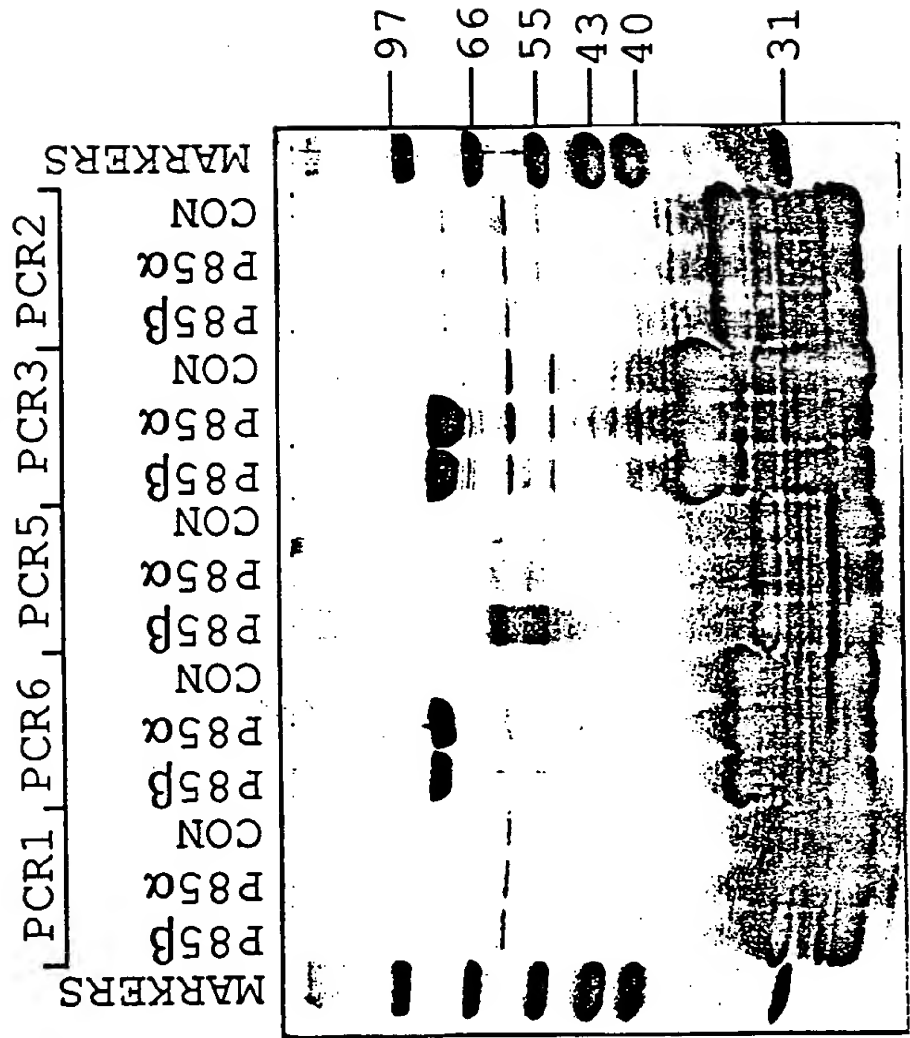


Figure 25 A

MAPPING THE P85 BINDING SITE ON P110



MAPPING THE P85 BINDING SITE ON P110 (2)

